

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/797788

CRF Processing Date: _____
 Edited by: _____
 Verified by: _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☒ Other: Corrected invalid amino acid numbering

FCT09

RAW SEQUENCE LISTING

DATE: 04/12/2001

PATENT APPLICATION: US/09/744,788

TIME: 11:46:09

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04122001\I744788.raw

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3 <110> APPLICANT: Yu, Kin Tak
4     Thrower, Larry W.
5     Labaudiniere, Richard F.
7 <120> TITLE OF INVENTION: ISOFORMS OF HUMAN CALCIUM SENSING RECEPTOR
9 <130> FILE REFERENCE: A2996-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/744,788
C--> 12 <141> CURRENT FILING DATE: 2001-01-30
14 <160> NUMBER OF SEQ ID NOS: 12
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 21
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
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27 <210> SEQ ID NO: 2
28 <211> LENGTH: 21
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37 <211> LENGTH: 21
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
41 <400> SEQUENCE: 3
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46 <211> LENGTH: 21
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48 <213> ORGANISM: Homo sapiens
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59 <400> SEQUENCE: 5
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72 <210> SEQ ID NO: 7
73 <211> LENGTH: 3003

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74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
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79 <222> LOCATION: (1)..(3003)
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83 Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
84 1 5 10 15
86 acc tct gcc tac ggg cca gac cag cga gcc caa aag aag ggg gac att 96
87 Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
88 20 25 30
90 atc ctt ggg ggg ctc ttt cct att cat ttt gga gta gca gct aaa gat 144
91 Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
92 35 40 45
94 caa gat ctc aaa tca agg ccg gag tct gtg gaa tgt atc agg tat aat 192
95 Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
96 50 55 60
98 ttc cgt ggg ttt cgc tgg tta cag gct atg ata ttt gcc ata gag gag 240
99 Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
100 65 70 75 80
102 ata aac agc agc cca gcc ctt ctt ccc aac ttg acg ctg gga tac agg 288
103 Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
104 85 90 95
106 ata ttt gac act tgc aac acc gtt tct aag gcc ttg gaa gcc acc ctg 336
107 Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
108 100 105 110
110 agt ttt gtt gct caa aac aaa att gat tct ttg aac ctt gat gag ttc 384
111 Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
112 115 120 125
114 tgc aac tgc tca gag cac att ccc tct acg att gct gtg gtg gga gca 432
115 Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
116 130 135 140
118 act ggc tca ggc gtc tcc acg gca gtg gca aat ctg ctg ggg ctc ttc 480
119 Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
120 145 150 155 160
122 tac att ccc cag gtc agt tat gcc tcc tcc agc aga ctc ctc agc aac 528
123 Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
124 165 170 175
126 aag aat caa ttc aag tct ttc ctc cga acc atc ccc aat gat gag cac 576
127 Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
128 180 185 190
130 cag gcc act gcc atg gca gac atc atc gag tat ttc cgc tgg aac tgg 624
131 Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
132 195 200 205
134 gtg ggc aca att gca gct gat gac gac tat ggg cgg ccg ggg att gag 672
135 Val Gly Thr Ile Ala Ala Asp Asp Tyr Gly Arg Pro Gly Ile Glu
136 210 215 220
138 aaa ttc cga gag gaa gct gag gaa agg gat atc tgc atc gac ttc agt 720

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139	Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	Phe	Ser	
140	225					230					235					240	
142	gaa	ctc	atc	tcc	cag	tac	tct	gat	gag	gaa	gag	atc	cag	cat	gtg	gta	768
143	Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	His	Val	Val	
144				245					250						255		
146	gag	gtg	att	caa	aat	tcc	acg	gcc	aaa	gtc	atc	gtg	gtt	ttc	tcc	agt	816
147	Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	Val	Phe	Ser	Ser	
148				260					265					270			
150	ggc	cca	gat	ctt	gag	ccc	ctc	atc	aag	gag	att	gtc	cgg	cgc	aat	atc	864
151	Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	Arg	Arg	Asn	Ile	
152			275					280					285				
154	acg	ggc	aag	atc	tgg	ctg	gcc	agc	gag	gcc	tgg	gcc	agc	tcc	tcc	ctg	912
155	Thr	Gly	Lys	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser	Ser	Leu	
156		290				295					300						
158	atc	gcc	atg	cct	cag	tac	ttc	cac	gtg	gtt	ggc	ggc	acc	att	gga	ttc	960
159	Ile	Ala	Met	Pro	Gln	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile	Gly	Phe	
160	305				310					315					320		
162	gct	ctg	aag	gct	ggg	cag	atc	cca	ggc	ttc	cgg	gaa	ttc	ctg	aag	aag	1008
163	Ala	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	Phe	Leu	Lys	Lys	
164				325					330					335			
166	gtc	cat	ccc	agg	aag	tct	gtc	cac	aat	ggt	ttt	gcc	aag	gag	ttt	tgg	1056
167	Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	Lys	Glu	Phe	Trp	
168			340					345					350				
170	gaa	gaa	aca	ttt	aac	tgc	cac	ctc	caa	gaa	ggt	gca	aaa	gga	cct	tta	1104
171	Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	Lys	Gly	Pro	Leu	
172		355				360					365						
174	cct	gtg	gac	acc	ttt	ctg	aga	ggt	cac	gaa	gaa	agt	ggc	gac	agg	ttt	1152
175	Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	Gly	Asp	Arg	Phe	
176		370				375					380						
178	agc	aac	agc	tgc	aca	gcc	ttc	cga	ccc	ctc	tgt	aca	ggg	gat	gag	aac	1200
179	Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn	
180	385				390				395					400			
182	atc	agc	agt	gtc	gag	acc	cct	tac	ata	gat	tac	acg	cat	tta	cgg	ata	1248
183	Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Ile	Asp	Tyr	Thr	His	Leu	Arg	Ile	
184				405					410				415				
186	tcc	tac	aat	gtg	tac	tta	gca	gtc	tac	tcc	att	gcc	cac	gcc	ttg	caa	1296
187	Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln	
188			420					425				430					
190	gat	ata	tat	acc	tgc	tta	cct	ggg	aga	ggg	ctc	ttc	acc	aat	ggc	tcc	1344
191	Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser	
192		435				440					445						
194	tgt	gca	gac	atc	aag	aaa	gtt	gag	gcg	tgg	cag	gtg	ccc	ttc	tcc	aac	1392
195	Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Pro	Phe	Ser	Asn	
196		450				455					460						
198	tgc	agc	cga	gac	tgc	ctg	gca	ggg	acc	agg	aaa	ggg	atc	att	gag	ggg	1440
199	Cys	Ser	Arg	Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	
200	465				470				475				480				
202	gag	ccc	acc	tgc	tgc	ttt	gag	tgt	gtg	gag	tgt	cct	gat	ggg	gag	tat	1488
203	Glu	Pro	Thr	Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	

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204		485		490		495		
206	agt gat gag aca gat gcc agt gcc tgt aac aag tgc cca gat gac ttc							1536
207	Ser Asp Glu Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe							
208		500		505		510		
210	tgg tcc aat gag aac cac acc tcc tgc att gcc aag gag atc gag ttt							1584
211	Trp Ser Asn Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe							
212		515		520		525		
214	ctg tgc tgg acg gag ccc ttt ggg atc gca ctc acc ctc ttt gcc gtg							1632
215	Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val							
216		530		535		540		
218	ctg ggc att ttc ctg aca gcc ttt gtg ctg ggt gtg ttt atc aag ttc							1680
219	Leu Gly Ile Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe							
220	545	550		555		560		
222	cgc aac aca ccc att gtc aag gcc acc aac cga gag ctc tcc tac ctc							1728
223	Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu							
224		565		570		575		
226	ctc ctc ttc tcc ctg ctc tgc tgc ttc tcc agc tcc ctg ttc ttc atc							1776
227	Leu Leu Phe Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile							
228		580		585		590		
230	ggg gag ccc cag gac tgg acg tgc cgc ctg cgc cag ccg gcc ttt ggc							1824
231	Gly Glu Pro Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly							
232		595		600		605		
234	atc agc ttc gtg ctc tgc atc tca tgc atc ctg gtg aaa acc aac cgt							1872
235	Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg							
236		610		615		620		
238	gtc ctc ctg gtg ttt gag gcc aag atc ccc acc agc ttc cac cgc aag							1920
239	Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys							
240	625	630		635		640		
242	tgg tgg ggg ctc aac ctg cag ttc ctg ctg gtt ttc ctc tgc acc ttc							1968
243	Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe							
244		645		650		655		
246	atg cag att gtc atc tgt gtg atc tgg ctc tac acc gcg ccc ccc tca							2016
247	Met Gln Ile Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser							
248		660		665		670		
250	agc tac cgc aac cag gag ctg gag gat gag atc atc ttc atc acg tgc							2064
251	Ser Tyr Arg Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys							
252		675		680		685		
254	cac gag ggc tcc ctc atg gcc ctg ggc ttc ctg atc ggc tac acc tgc							2112
255	His Glu Gly Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys							
256		690		695		700		
258	ctg ctg gct gcc atc tgc ttc ttc ttt gcc ttc aag tcc cgg aag ctg							2160
259	Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu							
260	705	710		715		720		
262	ccg gag aac ttc aat gaa gcc aag ttc atc acc ttc agc atg ctc atc							2208
263	Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile							
264		725		730		735		
266	ttc ttc atc gtc tgg atc tcc ttc att cca gcc tat gcc agc acc tat							2256
267	Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr							
268		740		745		750		

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270 ggc aag ttt gtc tct gcc gta gag gtg att gcc atc ctg gca gcc agc 2304
271 Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser
272      755      760      765
274 ttt ggc ttg ctg gcg tgc atc ttc ttc aac aag atc tac atc att ctc 2352
275 Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile Leu
276      770      775      780
278 ttc aag cca tcc cgc aac acc atc gag gag gtg cgt tgc agc acc gca 2400
279 Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala
280 785      790      795      800
282 gct cac gct ttc aag gtg gct gcc cgg gcc acg ctg cgc cgc agc aac 2448
283 Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn
284      805      810      815
286 gtc tcc cgc aag cgg tcc agc agc ctt gga ggc tcc acg gga tcc acc 2496
287 Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr
288      820      825      830
290 cct tcc tcc tcc atc agc agc aag agc aac agc gaa gac cca ttc cca 2544
291 Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro
292      835      840      845
294 cag ccc gag agg cag aag cag cag caq ccg ctg gcc cta acc cag caa 2592
295 Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln
296      850      855      860
298 gag cag cag cag cag ccc ctg acc ctc cca cag cag caa cga tct cag 2640
299 Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln
300 865      870      875      880
302 cag cag ccc aga tgc aag cag aag gtc atc ttt ggc agc ggc acg gtc 2688
303 Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val
304      885      890      895
306 acc ttc tca ctg agc ttt gat gag cct cag aag aac gcc atg gcc cac 2736
307 Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His
308      900      905      910
310 agg aat tct acg cac cag aac tcc ctg gag gcc cag aaa agc agc gat 2784
311 Arg Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp
312      915      920      925
314 acg ctg acc cga cac cag cca tta ctc ccg ctg cag tgc ggg gaa acg 2832
315 Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr
316      930      935      940
318 gac tta gat ctg acc gtc cag gaa aca ggt ctg caa gga cct gtg ggt 2880
319 Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly
320 945      950      955      960
322 gga gac cag cgg cca gag gtg gag gac cct gaa gag ttg tcc cca gca 2928
323 Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala
324      965      970      975
326 ctt gta gtg tcc agt tca cag agc ttt gtc atc agt ggt gga ggc agc 2976
327 Leu Val Val Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser
328      980      985      990
330 act gtt aca gaa aac gta gtg aat tca / 3003
331 Thr Val Thr Glu Asn Val Val Asn Ser
332      995      1000
335 <210> SEQ ID NO: 8

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date